

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Coleman, Roger  
Au-Young, Janice  
Bandman, Olga  
Seilhamer, Jeffrey J.
- (ii) TITLE OF INVENTION: C5a-Like Seven Transmembrane Receptor
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
  - (B) STREET: 3330 Hillview Avenue
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Luther, Barbara J.
  - (B) REGISTRATION NUMBER: 33954
  - (C) REFERENCE/DOCKET NUMBER: PF-0040 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-852-0195

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1446 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: Mast Cell

(B) CLONE: 8118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCGTCTT TCTCTGCTGA GACCAATTCA ACTGACCTAC TCTCACAGCC ATGGAATGAG	60
CCCCCAGTAA TTCTCTCCAT GGTCATTCTC AGCCTTACTT TTTTACTGGG ATTGCCAGGC	120
AATGGGCTGG TGCTGTGGGT GGCTGGCCTG AAGATGCAGC GGACAGTGAA CACAATTTGG	180
TTCCTCCACC TCACCTTGGC GGACCTCCTC TGCTGCCTCT CCTTGGCCTT CTCGCTGGCT	240
CACTTGGCTC TCCAGGGACA GTGGCCCTAC GGCAGGTTCC TATGCAAGCT CATCCCCTCC	300
ATCATTGTCC TCAACATGTT TGGCAGTGTC TTCCTGCTTA CTGCCATTAG CCTGGATCGC	360
TGTCTTGTGG TATTCAAGCC AATCTGGTGT CAGATTCATC GCAATGTAGG GATGGCCTGC	420
TCTATCTGTG GATGTATCTG GGTGGTGGCT TTTGTGTTGT GCATTCTGT GTTCGTGTAC	480
CGGGAAATCT TCACTACAGA CAACCATAAT AGATGTGGCT ACAAATTTGG TCTCTCCAGC	540
TCATTAGATT ATCCAGACTT TTATGGGGAT CCACTAGAAA ACAGGTCTCT TGAAAACATT	600
GTTCAGCCGC CTGGAGAAAT GAATGATAGG TTAGATCCTT CCTCTTTCCA AACAAATGAT	660
CATCCTTGGA CAGTCCCCAC TGTCTTCCAA CCTCAAACAT TTCAAAGACC TTCTGCAGAT	720
TCACTCCCTA GGGGTTCTGC TAGGTTAACA AGTCAAAATC TGTATTCTAA TGTATTTAAA	780
CCTGCTGATG TGGTCTCACC TAAAATCCCC AGTGGGTTTC CTATTGAAGA TCACGAAACC	840
AGCCCACTGG ATAACTCTGA TGCTTTTCTC TCTACTCATT TAAAGCTGTT CCCTAGCGCT	900
TCTAGCAATT CCTTCTACGA GTCTGAGCTA CCACAAGGTT TCCAGGATTA TTACAATTTA	960
GGCCAATTCA CAGATGACGA TCAAGTGCCA ACACCCCTCG TGGCAATAAC GATCACTAGG	1020
CTAGTGGTGG GTTTCCTGCT GCCCTCTGTT ATCATGATAG CCTGTTACAG CTTTATTGTC	1080
TTCCGAATGC AAAGGGGCGG CTTGCGCAAG TCTCAGAGCA AAACCTTTTCG AGTGGCCGTG	1140
GTGGTGGTGG CTGTCTTTCT TGTCTGCTGG ACTCCATACC ACATTTGGGG AGTCCTGTCA	1200
TTGCTTACTG ACCCAGAAAC TCCCTTGGGG AAAACTCTGA TGTCTGGGA TCATGTATGC	1260
ATTGCTCTAG CATCTGCCAA TAGTTGCTTT AATCCCTTCC TTTATGCCCT CTTGGGGAAA	1320
GATTTTAGGA AGAAAGCAAG GCAGTCCATT CAGGGAATTC TGGAGGCAGC CTTCAGTGAG	1380
GAGCTCACAC GTTCCACCCA CTGTCCCTCA AACAATGTCA TTTCAGAAAG AAATAGTACA	1440
ACTGTG	1446

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Phe Ser Ala Glu Thr Asn Ser Thr Asp Leu Leu Ser Gln  
1 5 10 15  
Pro Trp Asn Glu Pro Pro Val Ile Leu Ser Met Val Ile Leu Ser Leu  
20 25 30  
Thr Phe Leu Leu Gly Leu Pro Gly Asn Gly Leu Val Leu Trp Val Ala  
35 40 45  
Gly Leu Lys Met Gln Arg Thr Val Asn Thr Ile Trp Phe Leu His Leu  
50 55 60  
Thr Leu Ala Asp Leu Leu Cys Cys Leu Ser Leu Ala Phe Ser Leu Ala  
65 70 75 80  
His Leu Ala Leu Gln Gly Gln Trp Pro Tyr Gly Arg Phe Leu Cys Lys  
85 90 95  
Leu Ile Pro Ser Ile Ile Val Leu Asn Met Phe Gly Ser Val Phe Leu  
100 105 110  
Leu Thr Ala Ile Ser Leu Asp Arg Cys Leu Val Val Phe Lys Pro Ile  
115 120 125  
Trp Cys Gln Asn His Arg Asn Val Gly Met Ala Cys Ser Ile Cys Gly  
130 135 140  
Cys Ile Trp Val Val Ala Phe Val Leu Cys Ile Pro Val Phe Val Tyr  
145 150 155 160  
Arg Glu Ile Phe Thr Thr Asp Asn His Asn Arg Cys Gly Tyr Lys Phe  
165 170 175  
Gly Leu Ser Ser Ser Leu Asp Tyr Pro Asp Phe Tyr Gly Asp Pro Leu  
180 185 190  
Glu Asn Arg Ser Leu Glu Asn Ile Val Gln Pro Pro Gly Glu Met Asn  
195 200 205  
Asp Arg Leu Asp Pro Ser Ser Phe Gln Thr Asn Asp His Pro Trp Thr  
210 215 220  
Val Pro Thr Val Phe Gln Pro Gln Thr Phe Gln Arg Pro Ser Ala Asp  
225 230 235 240  
Ser Leu Pro Arg Gly Ser Ala Arg Leu Thr Ser Gln Asn Leu Tyr Ser  
245 250 255  
Asn Val Phe Lys Pro Ala Asp Val Val Ser Pro Lys Ile Pro Ser Gly  
260 265 270

Phe Pro Ile Glu Asp His Glu Thr Ser Pro Leu Asp Asn Ser Asp Ala  
 275 280 285  
 Phe Leu Ser Thr His Leu Lys Leu Phe Pro Ser Ala Ser Ser Asn Ser  
 290 295 300  
 Phe Tyr Glu Ser Glu Leu Pro Gln Gly Phe Gln Asp Tyr Tyr Asn Leu  
 305 310 315 320  
 Gly Gln Phe Thr Asp Asp Asp Gln Val Pro Thr Pro Leu Val Ala Ile  
 325 330 335  
 Thr Ile Thr Arg Leu Val Val Gly Phe Leu Leu Pro Ser Val Ile Met  
 340 345 350  
 Ile Ala Cys Tyr Ser Phe Ile Val Phe Arg Met Gln Arg Gly Arg Phe  
 355 360 365  
 Ala Lys Ser Gln Ser Lys Thr Phe Arg Val Ala Val Val Val Val Ala  
 370 375 380  
 Val Phe Leu Val Cys Trp Thr Pro Tyr His Ile Trp Gly Val Leu Ser  
 385 390 395 400  
 Leu Leu Thr Asp Pro Glu Thr Pro Leu Gly Lys Thr Leu Met Ser Trp  
 405 410 415  
 Asp His Val Cys Ile Ala Leu Ala Ser Ala Asn Ser Cys Phe Asn Pro  
 420 425 430  
 Phe Leu Tyr Ala Leu Leu Gly Lys Asp Phe Arg Lys Lys Ala Arg Gln  
 435 440 445  
 Ser Ile Gln Gly Ile Leu Glu Ala Ala Phe Ser Glu Glu Leu Thr Arg  
 450 455 460  
 Ser Thr His Cys Pro Ser Asn Asn Val Ile Ser Glu Arg Asn Ser Thr  
 465 470 475 480  
 Thr Val